

SEQUENCE LISTING

<110> TANABE, TADASHI
YOKOYAMA, CHIEKO

<120> ANTIBODIES SPECIFIC TO HUMAN PROSTACYCLIN SYNTHASE

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<151> 2000-09-27

<150> 09/037,758

<151> 1998-01-10

<150> 08/578,706

<151> 1995-12-28

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<170> PatentIn Ver. 2.1

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 1

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<220>
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<223> Inosine

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 cta tcc cca gcc agg ctg gcc agg cgg gcc cac cgg agc aaa tgg ctg 96
 Leu Ser Pro Ala Arg Leu Ala Arg Arg Ala His Arg Ser Lys Trp Leu
 20 25 30
 gag agt tac ctg ctg cac ctg gag gag atg ggt gtg tca gag gag atg 144
 Glu Ser Tyr Leu Leu His Leu Glu Glu Met Gly Val Ser Glu Glu Met
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 <212> PRT
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Met Ala Trp Ala Ala Leu Leu Gly Leu Leu Ala																	
1 5 10																	
gca ctg ttg ctg ctg ctg cta ctg agc cgc cgc cgc acg cgg cga cct																	160
Ala Leu Leu Leu Leu Leu Leu Leu Ser Arg Arg Arg Thr Arg Arg Pro																	
15 20 25																	
ggt gag cct ccc ctg gac ctg ggc agc atc ccc tgg ttg ggg tat gcc																	208
Gly Glu Pro Pro Leu Asp Leu Gly Ser Ile Pro Trp Leu Gly Tyr Ala																	
30 35 40																	
ttg gac ttt gga aaa gat gct gcc agc ttc ctc acg agg atg aag gag																	256
Leu Asp Phe Gly Lys Asp Ala Ala Ser Phe Leu Thr Arg Met Lys Glu																	
45 50 55																	
aag cac ggt gac atc ttt act ata ctg gtt ggg ggc agg tat gtc acc																	304
Lys His Gly Asp Ile Phe Thr Ile Leu Val Gly Gly Arg Tyr Val Thr																	
60 65 70 75																	
gtt ctc ctg gac cca cac tcc tac gac gcg gtg gtg tgg gag cct cgc																	352
Val Leu Leu Asp Pro His Ser Tyr Asp Ala Val Val Trp Glu Pro Arg																	
80 85 90																	
acc agg ctc gac ttc cat gcc tat gcc atc ttc ctc atg gag agg att																	400
Thr Arg Leu Asp Phe His Ala Tyr Ala Ile Phe Leu Met Glu Arg Ile																	
95 100 105																	
ttt gat gtg cag ctt cca cat tac agc ccc agt gat gaa aag gcc agg																	448
Phe Asp Val Gln Leu Pro His Tyr Ser Pro Ser Asp Glu Lys Ala Arg																	
110 115 120																	
atg aaa ctg act ctt ctc cac aga gag ctc cag gca ctc aca gaa gcc																	496
Met Lys Leu Thr Leu Leu His Arg Glu Leu Gln Ala Leu Thr Glu Ala																	
125 130 135																	
atg tat acc aac ctc cat gca gtg ctg ttg ggc gat gct aca gaa gca																	544
Met Tyr Thr Asn Leu His Ala Val Leu Leu Gly Asp Ala Thr Glu Ala																	
140 145 150 155																	
ggc agt ggc tgg cac gag atg ggt ctc ctc gac ttc tcc tac agc ttc																	592
Gly Ser Gly Trp His Glu Met Gly Leu Leu Asp Phe Ser Tyr Ser Phe																	
160 165 170																	

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175 180 185	
cgc acc cat gaa agc cag gcc cag gac cgc gtc cac tca gct gat gtc	688
Arg Thr His Glu Ser Gln Ala Gln Asp Arg Val His Ser Ala Asp Val	
190 195 200	
ttc cac acc ttt cgc cag ctc gac cgg ctg ctc ccc aaa ctg gcc cgt	736
Phe His Thr Phe Arg Gln Leu Asp Arg Leu Leu Pro Lys Leu Ala Arg	
205 210 215	
ggc tcc ctg tca gtg ggg gac aag gac cac atg tgc agt gtc aaa agt	784
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Arg Leu	

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Asp	Leu	Gly	Ser	Ile	Pro	Trp	Leu	Gly	Tyr	Ala	Leu	Asp	Phe	Gly	Lys	
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Asp	Ala	Ala	Ser	Phe	Leu	Thr	Arg	Met	Lys	Glu	Lys	His	Gly	Asp	Ile	
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Phe	Thr	Ile	Leu	Val	Gly	Gly	Arg	Tyr	Val	Thr	Val	Leu	Leu	Asp	Pro	
	65				70					75					80	
His	Ser	Tyr	Asp	Ala	Val	Val	Trp	Glu	Pro	Arg	Thr	Arg	Leu	Asp	Phe	
				85					90					95		
His	Ala	Tyr	Ala	Ile	Phe	Leu	Met	Glu	Arg	Ile	Phe	Asp	Val	Gln	Leu	
			100					105					110			
Pro	His	Tyr	Ser	Pro	Ser	Asp	Glu	Lys	Ala	Arg	Met	Lys	Leu	Thr	Leu	
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Leu	His	Arg	Glu	Leu	Gln	Ala	Leu	Thr	Glu	Ala	Met	Tyr	Thr	Asn	Leu	
	130					135					140					
His	Ala	Val	Leu	Leu	Gly	Asp	Ala	Thr	Glu	Ala	Gly	Ser	Gly	Trp	His	
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Glu	Met	Gly	Leu	Leu	Asp	Phe	Ser	Tyr	Ser	Phe	Leu	Leu	Arg	Ala	Gly	
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Tyr Leu Thr Leu Tyr Gly Ile Glu Ala Leu Pro Arg Thr His Glu Ser
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 Gln Ala Gln Asp Arg Val His Ser Ala Asp Val Phe His Thr Phe Arg
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 Leu Ser Pro Ala Arg Leu Ala Arg Arg Ala His Arg Ser Lys Trp Leu
 20 25 30
 gag agt tac ctg ctg cac ctg gag gag atg ggt gtg tca gag gag atg 143
 Glu Ser Tyr Leu Leu His Leu Glu Glu Met Gly Val Ser Glu Glu Met
 35 40 45
 cag gca cgg gcc ctg gtg ctg cag ctg tgg gcc aca cag ggg aat atg 191
 Gln Ala Arg Ala Leu Val Leu Gln Leu Trp Ala Thr Gln Gly Asn Met
 50 55 60
 ggt ccc gct gcc ttc tgg ctc ctg ctc ttc ctt ctc aag aat cct gaa 239
 Gly Pro Ala Ala Phe Trp Leu Leu Leu Phe Leu Leu Lys Asn Pro Glu
 65 70 75
 gcc ctg gct gct gtc cgc gga gag ctc gag agt atc ctt tgg caa gcg 287
 Ala Leu Ala Ala Val Arg Gly Glu Leu Glu Ser Ile Leu Trp Gln Ala
 80 85 90 95
 gag cag cct gtc tgc cag acg acc act ctc cca cag aag gtt cta gac 335
 Glu Gln Pro Val Ser Gln Thr Thr Leu Pro Gln Lys Val Leu Asp
 100 105 110
 agc aca cct gtg ctt gat agc gtg ctg agt gag agc ctc agg ctt aca 383
 Ser Thr Pro Val Leu Asp Ser Val Leu Ser Glu Ser Leu Arg Leu Thr
 115 120 125

gct gcc ccc ttc atc acc cgc gag gtt gtg gtg gac ctg gcc atg ccc 431
 Ala Ala Pro Phe Ile Thr Arg Glu Val Val Val Asp Leu Ala Met Pro
 130 135 140

atg gca gac ggg aga gaa ttc aac ctg cga cgt ggt gac cgc ctc ctc 479
 Met Ala Asp Gly Arg Glu Phe Asn Leu Arg Arg Gly Asp Arg Leu Leu
 145 150 155

ctc ttc ccc ttc ctg agc ccc cag aga gac cca gaa atc tac aca gac 527
 Leu Phe Pro Phe Leu Ser Pro Gln Arg Asp Pro Glu Ile Tyr Thr Asp
 160 165 170 175

cca gag gta ttt aaa tac aac cga ttc ctg aac cct gac gga tca gag 575
 Pro Glu Val Phe Lys Tyr Asn Arg Phe Leu Asn Pro Asp Gly Ser Glu
 180 185 190

aag aaa gac ttt tac aag gat ggg aaa cgg ctg aag aat tac aac atg 623
 Lys Lys Asp Phe Tyr Lys Asp Gly Lys Arg Leu Lys Asn Tyr Asn Met
 195 200 205

ccc tgg ggg gcg ggg cac aat cac tgc ctg ggg agg agt tat gcg gtc 671
 Pro Trp Gly Ala Gly His Asn His Cys Leu Gly Arg Ser Tyr Ala Val
 210 215 220

aac agc atc aaa caa ttt gtg ttc ctt gtg ctg gtg cac ttg gac ttg 719
 Asn Ser Ile Lys Gln Phe Val Phe Leu Val Leu Val His Leu Asp Leu
 225 230 235

gag ctg atc aac gca gat gtg gag atc cct gag ttt gac ctc agc agg 767
 Glu Leu Ile Asn Ala Asp Val Glu Ile Pro Glu Phe Asp Leu Ser Arg
 240 245 250 255

tac ggc ttc ggt ctg atg cag ccg gaa cac gac gtg ccc gtc cgc tac 815
 Tyr Gly Phe Gly Leu Met Gln Pro Glu His Asp Val Pro Val Arg Tyr
 260 265 270

cgc atc cgc cca tgacacaggg agcagatgga tccacgtgct cgcctctgcc 867
 Arg Ile Arg Pro
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<400> 13

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Ser	Tyr	Leu	Leu	His	Leu	Glu	Glu	Met	Gly	Val	Ser	Glu	Glu	Met	Gln	35	40	45	
Ala	Arg	Ala	Leu	Val	Leu	Gln	Leu	Trp	Ala	Thr	Gln	Gly	Asn	Met	Gly	50	55	60	
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Thr	Pro	Val	Leu	Asp	Ser	Val	Leu	Ser	Glu	Ser	Leu	Arg	Leu	Thr	Ala	115	120	125	
Ala	Pro	Phe	Ile	Thr	Arg	Glu	Val	Val	Val	Asp	Leu	Ala	Met	Pro	Met	130	135	140	
Ala	Asp	Gly	Arg	Glu	Phe	Asn	Leu	Arg	Arg	Gly	Asp	Arg	Leu	Leu	Leu	145	150	155	160
Phe	Pro	Phe	Leu	Ser	Pro	Gln	Arg	Asp	Pro	Glu	Ile	Tyr	Thr	Asp	Pro	165	170	175	
Glu	Val	Phe	Lys	Tyr	Asn	Arg	Phe	Leu	Asn	Pro	Asp	Gly	Ser	Glu	Lys	180	185	190	
Lys	Asp	Phe	Tyr	Lys	Asp	Gly	Lys	Arg	Leu	Lys	Asn	Tyr	Asn	Met	Pro	195	200	205	
Trp	Gly	Ala	Gly	His	Asn	His	Cys	Leu	Gly	Arg	Ser	Tyr	Ala	Val	Asn	210	215	220	
Ser	Ile	Lys	Gln	Phe	Val	Phe	Leu	Val	Leu	Val	His	Leu	Asp	Leu	Glu	225	230	235	240
Leu	Ile	Asn	Ala	Asp	Val	Glu	Ile	Pro	Glu	Phe	Asp	Leu	Ser	Arg	Tyr	245	250	255	

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Ile Arg Pro
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 Tyr Ala Leu Asp Phe Gly Lys Asp Ala Ala Ser Phe Leu Thr Arg Met
 45 50 55

aag gag aag cac ggt gac atc ttt act ata ctg gtt ggg ggc agg tat 246
 Lys Glu Lys His Gly Asp Ile Phe Thr Ile Leu Val Gly Gly Arg Tyr
 60 65 70

gtc acc gtt ctc ctg gac cca cac tcc tac gac gcg gtg gtg tgg gag 294
 Val Thr Val Leu Leu Asp Pro His Ser Tyr Asp Ala Val Val Trp Glu
 75 80 85

cct cgc acc agg ctc gac ttc cat gcc tat gcc atc ttc ctc atg gag 342
 Pro Arg Thr Arg Leu Asp Phe His Ala Tyr Ala Ile Phe Leu Met Glu
 90 95 100 105

agg att ttt gat gtg cag ctt cca cat tac agc ccc agt gat gaa aag 390
 Arg Ile Phe Asp Val Gln Leu Pro His Tyr Ser Pro Ser Asp Glu Lys
 110 115 120

gcc agg atg aaa ctg act ctt ctc cac aga gag ctc cag gca ctc aca 438
 Ala Arg Met Lys Leu Thr Leu Leu His Arg Glu Leu Gln Ala Leu Thr
 125 130 135

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 Glu Ala Met Tyr Thr Asn Leu His Ala Val Leu Leu Gly Asp Ala Thr
 140 145 150

gaa gca ggc agt ggc tgg cac gag atg ggt ctc ctc gac ttc tcc tac	534
Glu Ala Gly Ser Gly Trp His Glu Met Gly Leu Leu Asp Phe Ser Tyr	
155 160 165	
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Ser Phe Leu Leu Arg Ala Gly Tyr Leu Thr Leu Tyr Gly Ile Glu Ala	
170 175 180 185	
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Leu Pro Arg Thr His Glu Ser Gln Ala Gln Asp Arg Val His Ser Ala	
190 195 200	
gat gtc ttc cac acc ttt cgc cag ctc gac cgg ctg ctc ccc aaa ctg	678
Asp Val Phe His Thr Phe Arg Gln Leu Asp Arg Leu Leu Pro Lys Leu	
205 210 215	
gcc cgt ggc tcc ctg tca gtg ggg gac aag gac cac atg tgc agt gtc	726
Ala Arg Gly Ser Leu Ser Val Gly Asp Lys Asp His Met Cys Ser Val	
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aaa agt cgc ctg tgg aag ctg cta tcc cca gcc agg ctg gcc agg cgg	774
Lys Ser Arg Leu Trp Lys Leu Leu Ser Pro Ala Arg Leu Ala Arg Arg	
235 240 245	
gcc cac cgg agc aaa tgg ctg gag agt tac ctg ctg cac ctg gag gag	822
Ala His Arg Ser Lys Trp Leu Glu Ser Tyr Leu Leu His Leu Glu Glu	
250 255 260 265	
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Met Gly Val Ser Glu Glu Met Gln Ala Arg Ala Leu Val Leu Gln Leu	
270 275 280	
tgg gcc aca cag ggg aat atg ggt ccc gct gcc ttc tgg ctc ctg ctc	918
Trp Ala Thr Gln Gly Asn Met Gly Pro Ala Ala Phe Trp Leu Leu Leu	
285 290 295	
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Phe Leu Leu Lys Asn Pro Glu Ala Leu Ala Val Arg Gly Glu Leu	
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Glu Ser Ile Leu Trp Gln Ala Glu Gln Pro Val Ser Gln Thr Thr Thr	
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 Asp Pro Glu Ile Tyr Thr Asp Pro Glu Val Phe Lys Tyr Asn Arg Phe
 395 400 405

ctg aac cct gac gga tca gag aag aaa gac ttt tac aag gat ggg aaa 1302
 Leu Asn Pro Asp Gly Ser Glu Lys Lys Asp Phe Tyr Lys Asp Gly Lys
 410 415 420 425

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 Arg Leu Lys Asn Tyr Asn Met Pro Trp Gly Ala Gly His Asn His Cys
 430 435 440

ctg ggg agg agt tat gcg gtc aac agc atc aaa caa ttt gtg ttc ctt 1398
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 445 450 455

gtg ctg gtg cac ttg gac ttg gag ctg atc aac gca gat gtg gag atc 1446
 Val Leu Val His Leu Asp Leu Glu Leu Ile Asn Ala Asp Val Glu Ile
 460 465 470

cct gag ttt gac ctc agc agg tac ggc ttc ggt ctg atg cag ccg gaa 1494
 Pro Glu Phe Asp Leu Ser Arg Tyr Gly Phe Gly Leu Met Gln Pro Glu
 475 480 485

cac gac gtg ccc gtc cgc tac cgc atc cgc cca tgacacaggg agcagatgga 1547
 His Asp Val Pro Val Arg Tyr Arg Ile Arg Pro
 490 495 500

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gctgggtcca ggggagggaa aagctaagag ggtgaacaaa gaaaagacat tgaaagctct 1727

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<213> Homo sapiens

<400> 15

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10

15

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 Asp Ala Ala Ser Phe Leu Thr Arg Met Lys Glu Lys His Gly Asp Ile
 50 55 60
 Phe Thr Ile Leu Val Gly Gly Arg Tyr Val Thr Val Leu Leu Asp Pro
 65 70 75 80
 His Ser Tyr Asp Ala Val Val Trp Glu Pro Arg Thr Arg Leu Asp Phe
 85 90 95
 His Ala Tyr Ala Ile Phe Leu Met Glu Arg Ile Phe Asp Val Gln Leu
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 Pro His Tyr Ser Pro Ser Asp Glu Lys Ala Arg Met Lys Leu Thr Leu
 115 120 125
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 130 135 140
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 145 150 155 160
 Glu Met Gly Leu Leu Asp Phe Ser Tyr Ser Phe Leu Leu Arg Ala Gly
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 Tyr Leu Thr Leu Tyr Gly Ile Glu Ala Leu Pro Arg Thr His Glu Ser
 180 185 190
 Gln Ala Gln Asp Arg Val His Ser Ala Asp Val Phe His Thr Phe Arg
 195 200 205
 Gln Leu Asp Arg Leu Leu Pro Lys Leu Ala Arg Gly Ser Leu Ser Val
 210 215 220
 Gly Asp Lys Asp His Met Cys Ser Val Lys Ser Arg Leu Trp Lys Leu
 225 230 235 240
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 245 250 255
 Glu Ser Tyr Leu Leu His Leu Glu Glu Met Gly Val Ser Glu Glu Met
 260 265 270
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 275 280 285
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<223> Description of Artificial Sequence: Primer

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<223> Description of Artificial Sequence: Primer

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<223> Description of Artificial Sequence: Synthetic
peptide

<400> 18
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1 5 10

<210> 19
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<400> 19
Gly Val Glu Ala Pro Pro His Thr Gln Glu Ser Gln
1 5 10

<210> 20
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 20
Glu Cys Gly Ile Glu Ala Leu Pro Arg Thr His Glu Ser Gln
1 5 10